

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: JOHNSON, EUGENE M
MILBRANDT, JEFFREY D
KOTZBAUER, PAUL T
LAMPE, PATRICIA A
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DESAUVAGE, FRED

(ii) TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 242

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/220,617
(B) FILING DATE: 24 Dec. 1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: GENDLOFF, ELIE H.
(B) REGISTRATION NUMBER: 44,704
(C) REFERENCE/DOCKET NUMBER: 6029-7976

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
1 5 10 15
Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
20 25 30

Sub
E14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Gly Ala Arg Pro Xaa Gly Leu Arg Glu Leu Glu Val Ser Val Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "SERINE OR CYSTEINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Cys Ala Gly Ala Xaa Glu Ala Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ANY AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "GLUTAMINE OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Xaa Val Glu Ala Lys Pro Cys Cys Gly Pro Thr Ala Tyr Glu Asp
1 5 10 15

Xaa Val Ser Phe Leu Ser Val
20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Tyr His Thr Leu Gln Glu Leu Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala
85 90 95
Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val
100 105 110
Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg
115 120 125
Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly
130 135 140
Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe
165 170 175

Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg
180 185 190

Glu Cys Ala Cys Val
195

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 195 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
1 5 10 15

Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
20 25 30

Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
35 40 45

Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60

Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
65 70 75 80

Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro
85 90 95

Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu
100 105 110

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
115 120 125

Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg
130 135 140

Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His
145 150 155 160

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp
165 170 175

Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys
180 185 190

Ala Cys Val
195

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCGGTTGG GGGCGCGGCC TTGCGGGCTG CGCGAGCTGG AGGTGCGCGT GAGCGAGCTG	60
GGCCTGGGCT ACGCGTCCGA CGAGACGGTG CTGTTCCGCT ACTGCGCAGG CGCCTGCGAG	120
GCTGCCGCGC GCGTCTACGA CCTCGGGCTG CGACGACTGC GCCAGCGGCG GCGCCTGCGG	180
CGGGAGCGGG TGC GCGCGCA GCCCTGCTGC CGCCCGACGG CCTACGAGGA CGAGGTGTCC	240
TTCCTGGACG CGCACAGCCG CTACCACAG GTGCACGAGC TGTCGGCGCG CGAGTGCGCC	300
TGCGTG	306

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCGGGGGCTC GGCCTTGTTG GCTGCGCGAG CTCGAGGTGC GCGTGAGCGA GCTGGGCCTG	60
GGCTACACGT CGGATGAGAC CGTGCTGTTT CGTACTGCG CAGGCGCGTG CGAGGCGGCC	120
ATCCGCATCT ACGACCTGGG CCTTCGGCGC CTGCGCCAGC GGAGGCGCGT GCGCAGAGAG	180
CGGGCGCGGG CGCACCCGTG TTGTCGCCCG ACGGECTATG AGGACGAGGT GTCCTTCCTG	240
GACGTGCACA GCCGCTACCA CACGCTGCAA GAGCTGTGCG CGCGGGAGTG CGCGTGCGTG	300

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCACTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCCT GGACGCCCCG ATTGCCCGCC TGGCCCAGTA CCGTGCACTC	180

CTGCAGGGGG CCCC GGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC	240
CCAGGTCCGC GCCGTGCGGC GGGGCCCCGG CGGCGGCGCG CGCGTGCGCG GTTGGGGGCG	300
CGGCCTTGCG GGCTGCGCGA GCTGGAGGTG CGCGTGAGCG AGCTGGGCCT GGGCTACGCG	360
TCCGACGAGA CGGTGCTGTT CCGCTACTGC GCAGGCGCCT GCGAGGCTGC CGCGCGCGTC	420
TACGACCTCG GGCTGCGACG ACTGCGCCAG CGGCGGCGCC TCGGCGGGA GCGGGTGCGC	480
GCGCAGCCCT GCTGCCGCCC GACGGCCTAC GAGGACGAGG TGTCC'TTCCT GGACGCGCAC	540
AGCCGCTACC ACACGGTGCA CGAGCTGTCG GCGCGCGAGT GCGCCTGCGT GTGA	594

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 588 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCT GGACGCCCGC ATCGCCCCGC TGGCCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAAGTTT CTCCCTGGGC TGCCCGCATC	240
CCGGGACCGC GCCGTGAGC GGTCCCCGG CGTCGCGGG CGCGGCCGGG GGCTCGGCCT	300
TGTGGGCTGC GCGAGCTCGA GGTGCGCGTG AGCGAGCTGG GCCTGGGCTA CACGTCGGAT	360
GAGACCGTGC TGTTCGCTA CTGCGCAGGC GCGTGCGAGG CGGCCATCCG CATCTACGAC	420
CTGGGCCTTC GCGCCTGCG CCAGCGGAGG CGCGTGCGCA GAGAGCGGGC GCGGGCGCAC	480
CCGTGTTGTC GCCCGACGGC CTATGAGGAC GAGGTGTCTT TCCTGGACGT GCACAGCCGC	540
TACCACACGC TGCAAGAGCT GTCGGCGCGG GAGTGCGCGT GCGTGTGA	588

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGCGGCTC CTCGCGTGGC	60
CCCGCGTCCT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCC	120

GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCGT 180
 GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCGGGTCCC 240
 CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG 300
 TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCCAGG 348

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTACCTCA CGCCCCCGA CCTGCGAAAG GGCCCTCCCT GCCGACCCTC GCTGAGAACT 60
 GACTTCACAT AAAGTGTGGG AACTCCC 87

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
 1 5 10 15
 Val Leu Ser

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
 1 5 10 15
 Leu Leu Ser

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCC

57

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCT

57

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile	Trp	Met	Cys	Arg	Glu	Gly	Leu	Leu	Leu	Ser	His	Arg	Leu	Gly	Pro	
1				5					10					15		
Ala	Leu	Val	Pro	Leu	His	Arg	Leu	Pro	Arg	Thr	Leu	Asp	Ala	Arg	Ile	
			20					25					30			
Ala	Arg	Leu	Ala	Gln	Tyr	Arg	Ala	Leu	Leu	Gln	Gly	Ala	Pro	Asp	Ala	
			35				40					45				
Met	Glu	Leu	Arg	Glu	Leu	Thr	Pro	Trp	Ala	Gly	Arg	Pro	Pro	Gly	Pro	
			50			55					60					
Arg	Arg	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Arg	Ala	Arg					
			65			70				75						

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTGGATGT GTCGAGAGGG CCTGCTTCTC AGCCACCGCC TCGGACCTGC GCTGGTCCCC	60
CTGCACCGCC TGCCTCGAAC CCTGGACGCC CGGATTGCCC GCCTGGCCCA GTACCGTGCA	120
CTCCTGCAGG GGGCCCCGGA TCGATGGAG CTGCGCGAGC TGACGCCCTG GGCTGGGCGG	180
CCCCCAGGTC CGCGCCGTCG GCGGGGGCCC CGGCGCGGC GCGCGCGT	228

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCTGGATGT GCCAGGAGGG TCTGCTCTTG GGCCACCGCC TGGGACCCGC GCTTGCCCCG	60
CTACGACGCC CTCCACGCAC CCTGGACGCC CGCATCGCCC GCCTGGCCCA GTATCGCGCT	120
CTGCTCCAGG GCGCCCCGA CGCGGTGGAG CTTGAGAAC TTTCTCCCTG GGCTGCCCCG	180
ATCCCGGGAC CGCGCCGTCG AGCGGGTCCC CGGCGTCGGC GGGCGCGG	228

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg Leu Gly Pro	
1 5 10 15	
Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp Ala Arg Ile	
20 25 30	
Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala	
35 40 45	
Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro	
50 55 60	

Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
1 5 10 15
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg
20 25 30
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Arg Arg Trp Lys Ala Ala Ala Leu Val Ser Leu Ile Cys Ser Ser
1 5 10 15
Leu Leu Ser Val Trp Met Cys Gln Glu Gly Leu Leu Leu Gly His Arg
20 25 30
Leu Gly Pro Ala Leu Ala Pro Leu Arg Arg Pro Pro Arg Thr Leu Asp
35 40 45
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
50 55 60
Pro Asp Ala Val Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile
65 70 75 80
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg
85 90 95

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120
CACCGCCTGC CTCGAACCCT GGACGCCCCG ATGCCCCGCC TGGCCCAGTA CCGTGCACTC	180
CTGCAGGGGG CCCCGGATGC GATGGAGCTG CGCGAGCTGA CGCCCTGGGC TGGGCGGCCC	240
CCAGGTCCGC GCCGTCGGGC GGGGCCCCGG CGGCGGCGCG CGCGT	285

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCT GGACGCCCCG ATCGCCCCGCC TGGCCCAGTA TCGCGCTCTG	180
CTCCAGGGCG CCCCCGACGC GGTGGAGCTT CGAGAAGTTT CTCCCTGGGC TGCCCGCATC	240
CCGGGACCGC GCCGTCGAGC GGGTCCCCGG CGTCGGCGGG CGCGG	285

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCAGCGCT GGAAGGCGGC GGCCTTGGCC TCAGTGCTCT GCAGCTCCGT GCTGTCCATC	60
TGGATGTGTC GAGAGGGCCT GCTTCTCAGC CACCGCCTCG GACCTGCGCT GGTCCCCCTG	120

CACCGCCTGC CTCGAACCCT GGACGCCCCG APTGCCCGCC TGGCCCAGT

169

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCGTGCACT CCTGCAGGGG GCCCCGGATG CGATGGAGCT GCGCGAGCTG ACGCCCTGGG	60
CTGGGCGGGCC CCCAGGTCCG CGCCGTCGGG CGGGGCCCCG GCGGCGGCGC GCGCGTGCGC	120
GGTTGGGGGC GCGGCCCTTGC GGGCTGCGCG AGCTGGAGGT GCGCGTGAGC GAGCTGGGCC	180
TGGGCTACGC GTCCGACGAG ACGGTGCTGT TCGCTACTG CGCAGGCGCC TGCAGGCTG	240
CCGCGCGCGT CTACGACCTC GGGCTGCGAC GACTGCGCCA GCGGCGGCGC CTGCGGCGGG	300
AGCGGGTGCG CGCGCAGCCC TGCTGCCGCC CGACGGCCTA CGAGGACGAG GTGTCCTTCC	360
TGGACGCGCA CAGCCGCTAC CACACGGTGC ACGAGCTGTC GCGCGCGAG TCGCCTGCG	420
TGTGA	425

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAGGCGCT GGAAGGCAGC GGCCCTGGTG TCGCTCATCT GCAGCTCCCT GCTATCTGTC	60
TGGATGTGCC AGGAGGGTCT GCTCTTGGGC CACCGCTGG GACCCGCGCT TGCCCCGCTA	120
CGACGCCCTC CACGCACCCT GGACGCCCCG ATCGCCCGCC TGGCCCAGT	169

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCGCGCTCT GCTCCAGGGC GCCCCGACG CGGTGGAGCT TCGAGAACTT TCTCCCTGGG 60
 CTGCCCCGCAT CCCGGGACCG CGCCGTCGAG CGGGTCCCCG GCGTCGGCGG GCGCGGCCGG 120
 GGGCTCGGCC TTGTGGGCTG CGCGAGCTCG AGGTGCGCGT GAGCGAGCTG GGCCTGGGCT 180
 ACACGTCGGA TGAGACCGTG CTGTTCCGCT ACTGCGCAGG CGCGTGCGAG GCGGCCATCC 240
 GCATCTACGA CCTGGGCCTT CGGCGCCTGC GCCAGCGGAG GCGCGTGCGC AGAGAGCGGG 300
 CGCGGGCGCA CCCGTGTTGT CGCCCGACGG CCTATGAGGA CGAGGTGTCC TTCCTGGACG 360
 TGCACAGCCG CTACCACACG CTGCAAGAGC TGTCGCGCGG GGAGTGCGCG TGCCTGTGA 419

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1				5					10				15		
Tyr	Ala	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
			20					25					30		
Glu	Ala	Ala	Ala	Arg	Val	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
			35				40						45		
Arg	Arg	Arg	Leu	Arg	Arg	Glu	Arg	Val	Arg	Ala	Gln	Pro	Cys	Cys	Arg
			50				55					60			
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Ala	His	Ser	Arg
					70					75				80	
Tyr	His	Thr	Val	His	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
				85					90						

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Cys	Gly	Leu	Arg	Glu	Leu	Glu	Val	Arg	Val	Ser	Glu	Leu	Gly	Leu	Gly
1				5					10				15		

Tyr	Thr	Ser	Asp	Glu	Thr	Val	Leu	Phe	Arg	Tyr	Cys	Ala	Gly	Ala	Cys
			20					25					30		
Glu	Ala	Ala	Ile	Arg	Ile	Tyr	Asp	Leu	Gly	Leu	Arg	Arg	Leu	Arg	Gln
		35					40					45			
Arg	Arg	Arg	Val	Arg	Arg	Glu	Arg	Ala	Arg	Ala	His	Pro	Cys	Cys	Arg
		50				55					60				
Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser	Arg
65					70					75					80
Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys		
			85						90						

(2) INFORMATION FOR SEQ ID NO:33:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC
ACID"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Val Xaa Xaa Leu Gly Leu Gly Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:34:

- ```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 15 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 2
    (D) OTHER INFORMATION: /note= "THREONINE OR GLUTAMIC ACID"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 3
    (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
```

(B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "THREONINE OR VALINE OR ISOLEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site

(B) LOCATION: 11

(D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Cys	Cys	Arg	Pro	Xaa	Ala	Xaa	Xaa	Asp	Xaa	Xaa	Ser	Phe	Leu	Asp
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1				5					10	

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe	Arg	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Ala
1				5					10	

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "ISOLEUCINE OR THREONINE OR VALINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 10

(D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys	Cys	Arg	Pro	Xaa	Ala	Xaa	Xaa	Asp	Xaa
1				5					10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala	Xaa	Xaa	Asp	Xaa	Xaa	Ser	Phe	Ileu	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu	Xaa	Xaa	Xaa	Phe	Arg	Tyr	Cys
1				5			

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: 1
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR THREONINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "LEUCINE OR VALINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 4
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTNWSNGANY TNGGNYTNGG NTA

23

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTYMGNTAYT GYDSNGGNDG NTGYGANKCN GC

32

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCNGMNTCRC ANSHNCCNSH RCARTANCKR AA

32

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCRTCNTCRW ANGCRYNGG NCKRCARCA

29

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TCNARRAANS WNAVNTCRTC NTCRWANGC

29

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GARRMNBTH TNTTYMGNTA YTG

23

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GARRMNBTH TNTTYMGNTA YTGYSNGGN DSNTGHGA

38

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1023 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGAGGGAGAG CGCGCGGTGG TTTCGTCCGT GTGCCCCGCG CCCGGCGCTC CTCGCGTGGC	60
CCCGCGTCTT GAGCGCGCTC CAGCCTCCCA CGCGCGCCAC CCCGGGGTTC ACTGAGCCCC	120
GCGAGCCCGG GGAAGACAGA GAAAGAGAGG CCAGGGGGGG AACCCCATGG CCCGGCCCCG	180
GTCCCGCACC CTGTGCGGTG GCCTCCTCCG GCACGGGGTC CCCGGGTCGC CTCGGTCCC	240
CGCGATCCGG ATGGCGCACG CAGTGGCTGG GGCCGGGCCG GGCTCGGGTG GTCGGAGGAG	300
TCACCACTGA CCGGGTCATC TGGAGCCCGT GGCAGGCCGA GGCCAGGAT GAGGCGCTGG	360
AAGGCAGCGG CCCTGGTGTC GCTCATCTGC AGTCCCTGTC TATCTGTCTG GATGTGCCAG	420
GAGGGTCTGC TCTTGGGCCA CCGCCTGGGA CCCGCGCTTG CCCCGCTACG ACGCCCTCCA	480
CGCACCTTGG ACGCCCGCAT CGCCCGCCTG GCCAGTATC GCGCTCTGCT CCAGGGCGCC	540
CCCAGCGCGG TGGAGCTTCG AGAACTTTCT CCCTGGGCTG CCCGCATCCC GGGACGCGC	600
CGTCGAGCGG GTCCCCGGCG TCGCGGGCG CGGCCGGGG CTCGGCCTTG TGGGCTGCGC	660
GAGCTCGAGG TGCGCGTGAG CGAGCTGGGC CTGGGCTACA CGTCGGATGA GACCGTGCTG	720
TTCCGCTACT GCGCAGGCGC GTGCGAGGCG GCCATCCGCA TCTACGACCT GGGCCTTCGG	780

CGCCTGCGCC AGCGGAGGCG CGTGCGCAGA GAGCGGGCGC GGGCGCACCC GTGTTGTCGC 840
 CCGACGGCCT ATGAGGACGA GGTGTCCTTC CTGGACGTGC ACAGCCGCTA CCACACGCTG 900
 CAAGAGCTGT CGGCGCGGGA GTGCGCGTGC GTGTGATGCT ACCTCACGCC CCCCACCTG 960
 CGAAAGGGCC CTCCCTGCCG ACCCTCGCTG AGAACTGACT TCACATAAAG TGTGGGAACT 1020
 CCC 1023

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CCNACNGCNT AYGARGA

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
1				5					10					15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
			20					25					30		
Asp	Ala	Ala	Glu	Thr	Thr	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
		35					40					45			
Asn	Arg	Arg	Leu	Val	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
		50				55				60					
Ile	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
65					70					75				80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85					90						

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ARYTCYTGNA RNGTHGRTA

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GACGAGGTGT CCTTCCTGGA CGTACACA

28

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 47 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAYGARGACG AGGTGTCCTT CCTGGACGTA CACAGCCGCT AYCAAYAC

47

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GCGGCCATCC GCATCTACGA CCTGGG

26

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CRTAGGCCGT CGGGCGRCAR CACGGGT

27

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGCCGAAGG CCCAGGTCGT AGATGCG

27

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGCTACTGCG CAGGCGCGTG CGARGCGGC

29

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGCCGACAGC TCTTGACGCG TRTGGA

27

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAGCTGGGCC TGGGCTACGC GTCCGACGAG

30

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGACGCGTA CCATGAGGCG CTGGAAGGCA GCGGCCCTG

39

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GACCATATGC CGGGGGCTCG GCCTTGTGG

29

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GACGGATCCG CATCACACGC ACGCGCACTC

30

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CAGCGACGAC GCGTGCGCAA AGAGCG

26

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TAGCGGCTGT GTACGTCCAG GAAGGACACC TCGT

34

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AAAAATCGGG GGTGYGTCTT A

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATGCCTGGC CTACYTTGTC A

21

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGGCGTCCC AMCAAGGGTC TTCG

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GCCAGTGGTG CCGTCGAGGC GGG

23

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GGCCCAGGAT GAGGCGCTGG AAGG

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCACTCCACT GCCTGAWATT CWACCCC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCATGTGATT ATCGACCATT CGGC

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ser	Pro	Asp	Lys	Gln	Met	Ala	Val	Leu	Pro	Arg	Arg	Glu	Arg	Asn	Arg
1					5				10					15	

Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ser Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu Arg Asn Arg
 1 5 10 15
 Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
 20 25 30
 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
 35 40 45
 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
 50 55 60
 Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr Met Tyr Asp
 65 70 75 80
 Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr Ser Asp Lys
 85 90 95
 Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser
 100 105 110
 Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
 115 120 125
 Lys Arg Cys Gly Cys Ile
 130

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45

Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys
 20 25 30
 Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg
 35 40 45
 Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr
 50 55 60
 Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro
 65 70 75 80
 Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TGCCGACTGT GGAGCCTGAC CCTACCA	60
GCTGAGCTGG GCCTGGGCTA TGCCTCGGAG	
GAGAAGGTCA TCTTCCGATA CTGTGCTG	120
GC AGCTGTCCCC AAGAGGCCCG TACCCAGCAC	
AGTCTGGTAC TGGCCCGGCT TCGAGGGCGG	180
GGTCGAGCCC ATGGCCGACC CTGCTGCCAG	
CCCACCAGCT ATGCTGATGT GACCTTCCTT	240
GATGATCAGC ACCATTGGCA GCAGCTGCCT	
CAGCTCTCAG CTGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TGCCGGCTGT GGAGCCTGAC CCTACCA	60
GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	
GAGAAGATTA TCTTCCGATA CTGTGCTGGC	120
AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG	180
GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	
CCCACCAGCT ATGCTGATGT GACCTTCCTT	240
GATGACCACC ACCATTGGCA GCAGCTGCCT	
CAGCTCTCAG CCGCAGCTTG TGGCTGT	267

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TGCCGGCTGT GGAGCCTGAC CCTACCA	60
GCTGAGCTTG GCCTGGGCTA TGCCTCAGAG	
GAGAAGATTA TCTTCCGATA CTGTGCTGGC	120
AGCTGTCCCC AAGAGGTCCG TACCCAGCAC	
AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG	180
GGTCGAGCTC ATGGCAGACC TTGCTGCCAG	
CCCACCAGCT ATGCTGATGT GACCTTCCTT	240
GATGACCACC ACCATTGGCA GCAGCTGCCT	
CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT	273

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30
 Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
 65 70 75 80
 Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
 85 90 95

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala	Glu	Leu	Gly	Leu	Gly
1				5				10					15		
Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys
			20					25					30		
Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
			35				40					45			
Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	Tyr
	50					55					60				
Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	Gln	His	His	Trp	Gln	Gln	Leu	Pro
65					70				75						80
Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly					
				85					90						

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGCCTCAGAG GAGAAGATTA TC

22

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ala Ser Glu Glu Lys Ile Ile
1 5

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AGTCGGGGTT GGGGTATGCC TCA

23

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TATGCCTCAG AGGAGAAGAT TATCTT

26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCTCAGAGGA GAAGATTATC TTCCGATACT GTGCTGGCAG CTGTCCCCAA GAGGTCCGTA	60
CCCAGCACAG TCTGGTGCTG GCCCGTCTTC GAGGGGAGGG TCGAGCTCAT GGCAGACCTT	120
GCTGCCAGCC CACCAGCTAT GCTGATGTGA CCTTCCTTGA TGACCACCAC CATTGGCAGC	180
AGCTGCCTCA GCTCTCAGCC GCAGCTTGTT GCTGTGGTGG CTGAAGGCGG CCAGCCTGGT	240
CTCTCAGAAT CACAAGCAAG AGGCAGCCTT TGAAAGGCTC AGGTGACGTT ATTAGAAACT	300
TGCATAGGAG AAGATTAAGA AGAGAAAGGG GACCTG	336

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Cys Cys Arg Pro Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp
 1 5 10 15

Asp

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Lys Asp
 1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCATCAAGGA AGGTCACATC AGCATA

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCACCACAGC CACAAGCTGC GGSTGAGAGC TG

32

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Ala Leu Ala Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:


```

GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC TCCCCAATTC      60
CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT AGGTAACAAC      120
CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT GACCCTACCA      180
GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTCCG AACTGTGCT      240
GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG GCTTCGAGGG      300
CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA TGTGACCTTC      360
CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC TTGTGGCTGT      420
GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCAAA GCATGAGACA GGCTGGGCTT      480
TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA GGGAAAGGAC      540
CAGG                                                                    544

```

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Gln
1           5           10           15
Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu Arg Gly Gln
20           25           30
Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp
35           40           45
Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu Pro Gln Leu
50           55           60
Ser Ala Ala Ala Cys Gly Cys Gly Gly
65           70

```

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TGCCGGCTGT GGAGCCTGAC CCTACCAGTG GCTGAGCTTG GCCTGGGCTA TGCCCTCAGAG 60
 GAGAAGATTA TCTTCCGATA CTGTGCTGGC AGCTGTCCCC AAGAGGTCCG TACCCAGCAC 120
 AGTCTGGTGC TGGCCCGTCT TCGAGGGCAG GGTGAGCTC ATGGCAGACC TTGCTGCCAG 180
 CCCACCAGCT ATGCTGATGT GACCTTCCTT GATGACCACC ACCATTGGCA GCAGCTGCCT 240
 CAGCTCTCAG CCGCAGCTTG TGGCTGTGGT GGCTGAAGGC GGCCAGCCTG GTCTCTCAGA 300
 ATCACAAGCA AGAGGCAGCC TTTGAAAGGC TCAGGTGACG TTATTAGAAA CTGTCATAGG 360
 AGAAGATTAA GAAGAGAAAG GGGACCTGAT T 391

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "SERINE, THREONINE, OR

ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC

ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "ASPARTIC ACID, GLUTAMIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "valine or aspartic acid"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Asp Xaa Xaa Xaa Phe Leu Asp Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Glu Gly Pro Gly Arg Pro Ile Arg Val Arg Ile Pro Gly Gly Leu Pro
1 5 10 15

Thr Pro Gln Phe Leu Leu Ser Lys Pro Ser Leu Cys Leu Thr Ile Leu
20 25 30

Leu Tyr Leu Ala Leu Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu
35 40 45

Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu
 50 55 60

Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala
 65 70 75 80

Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala
 85 90 95

Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro
 100 105 110

Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln
 115 120 125

Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 130 135 140

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ala Leu Pro Gly Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "THREONINE, GLUTAMIC ACID OR LYSINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "VALINE, LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "LEUCINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Glu Xaa Xaa Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "ARGININE OR GLUTAMINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "THREONINE, VALINE OR ISOLEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "ALANINE OR SERINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "TYROSINE OR PHENYLALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR ALANINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "GLUTAMIC ACID, ASPARTIC ACID OR NO AMINO ACID"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 12

(D) OTHER INFORMATION: /note= "SERINE OR THREONINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 16

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Cys	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Phe	Leu	Asp	Xaa
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GTNDGNGANY TGGGNYTGGG NTA

23

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GANBTNWCNT TYYTNGANG

19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GANBTNWCNT TYYTNGANGW

20

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTYMGNTAYT GYDSNGGNDG NTG

23

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GTNDGNGANY TGGGNYTNGG

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GTNDGNGANY TGGGNYTGGG NTT

23

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

WCNTCNARRA ANGWNAVNTC

20

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

WCNTCNARRA ANGWNAVNT

19

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CANSHNCCNS HRCARTANCK RAA

23

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CANSHNCCNS HRCARTANCK RAANA

25

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

D

(B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Val Xaa Xaa Leu Gly Leu Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "VALINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "THREONINE OR SERINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 7
 (D) OTHER INFORMATION: /note= "ASPARTIC ACID OR VALINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Xaa Xaa Xaa Phe Leu Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

Sub
E14
Cone 1

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 7

(D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Arg Tyr Cys Xaa Gly Xaa Cys
1 5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "ASPARTIC ACID OR GLUTAMIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Val Xaa Xaa Leu Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "THREONINE, SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "GLUTAMIC ACID OR ASPARTIC ACID"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Val Xaa Xaa Leu Gly Leu Gly Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "ISOLEUCINE OR LEUCINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8
 (D) OTHER INFORMATION: /note= "SERINE OR ALANINE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Xaa Phe Arg Tyr Cys Xaa Gly Xaa Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCCTTGCA CCCGAGCCTC	60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG	120
GCAGAGACTA GAGGGACCTG GACGCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC	180

```

TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT      240
AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT      300
GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG      360
ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCG      420
GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA      480
TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC      540
TTGTGGCTGT GGTGGCTGA                                                    559

```

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
1          5          10          15
Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
20         25         30
Ala Arg Leu Arg Arg Ala Leu Ser Gly Pro Cys Gln Leu Trp Ser Leu
35         40         45
Thr Leu Ser Val Ala Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys
50         55         60
Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys Pro Arg Gly Ala Arg Thr
65         70         75         80
Gln His Gly Leu Ala Leu Ala Arg Leu Gln Gly Gln Gly Arg Ala His
85         90         95
Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr Thr Asp Val Ala Phe Leu
100        105        110
Asp Asp Arg His Arg Trp Gln Arg Leu Pro Gln Leu Ser Ala Ala Ala
115        120        125
Cys Gly Cys Gly Gly
130

```

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

This sequence is intentionally skipped

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Cys 1	Val	Leu	Thr	Ala 5	Ile	His	Leu	Asn	Val 10	Thr	Asp	Leu	Gly	Leu 15	Gly
Tyr	Glu	Thr	Lys 20	Glu	Glu	Leu	Ile	Phe 25	Arg	Tyr	Cys	Ser	Gly 30	Ser	Cys
Glu	Ala	Ala 35	Glu	Thr	Met	Tyr	Asp 40	Lys	Ile	Leu	Lys	Asn 45	Leu	Ser	Arg
Ser	Arg 50	Arg	Leu	Thr	Ser	Asp 55	Lys	Val	Gly	Gln	Ala 60	Cys	Cys	Arg	Pro
Val 65	Ala	Phe	Asp	Asp	Asp 70	Leu	Ser	Phe	Leu	Asp 75	Asp	Ser	Leu	Val	Tyr 80
His	Ile	Leu	Arg	Lys 85	His	Ser	Ala	Lys	Arg 90	Cys	Gly	Cys			

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Leu Ser Leu
1 5 10 15

His Pro Ser Leu Gly Trp Val
20

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Ser Leu
1 5 10 15
His Leu Gly Leu Gly Trp Val
20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

AATCCCCAGG ACAGGCAGGG AAT

23

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGGTACCCAG ATCTTCAGCC ACCACAGCCA CAAGC

35

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGACTATCAT ATGGCCCACC ACCACCACCA CCACCACCAC GACGACGACG ACAAGGCCTT

60

GGCTGGTTCA TGCCGA

76

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGCTGTCACC ATGGCTGCAG GAAGACTTCG GA

32

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ala	Leu	Ala	Gly	Ser	Cys	Arg	Leu	Trp	Ser	Leu	Thr	Leu	Pro	Val	Ala
1				5					10					15	
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
			20					25					30		
Cys	Ala	Gly	Ser	Cys	Pro	Gln	Glu	Ala	Arg	Thr	Gln	His	Ser	Leu	Val
		35				40					45				
Leu	Ala	Arg	Leu	Arg	Gly	Arg	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys
		50			55						60				
Arg	Pro	Thr	Ala	Tyr	Glu	Asp	Glu	Val	Ser	Phe	Leu	Asp	Val	His	Ser
65				70					75					80	
Arg	Tyr	His	Thr	Leu	Gln	Glu	Leu	Ser	Ala	Arg	Glu	Cys	Ala	Cys	Val
			85					90					95		

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TAATACGACT CACTATAGGG GAA

23

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TCGTCTTCGT AAGCAGTCGG ACGGCAGCAG GGTGGCCAT GGGCTCGAC

49

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGCTGCCGTC CGACTGCTTA CGAAGACGA

29

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTTATGCTAG TTATTGCTCA GCGGT

25

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
 35 40 45
 Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
 50 55 60
 His Pro Cys Cys Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp
 65 70 75 80
 Asp Gln His His Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys
 85 90 95
 Gly Cys Gly Gly
 100

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CACATCAGCA TAGCTGGTGG GCTGGCAGCA CGGGTGAGCA CGAGCACGTT

50

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TGCTGCCAGC CCACCAGCTA TGCTG

25

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CCTCGGAGGA GAAGGTCATC TTC

23

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys	Cys	Val	Arg	Gln	Leu	Tyr	Ile	Asp	Phe	Arg	Lys	Asp	Leu	Gly	Trp
1				5					10					15	
Lys	Trp	Ile	His	Glu	Pro	Lys	Gly	Tyr	His	Ala	Asn	Phe	Cys	Leu	Gly
			20					25					30		
Pro	Cys	Pro	Tyr	Ile	Trp	Ser	Leu	Asp	Thr	Gln	Tyr	Ser	Lys	Val	Leu
		35				40						45			
Ala	Leu	Tyr	Asn	Gln	His	Asn	Pro	Gly	Ala	Ser	Ala	Ala	Pro	Cys	Cys
	50					55					60				
Val	Pro	Gln	Ala	Leu	Glu	Pro	Leu	Pro	Ile	Val	Tyr	Tyr	Val	Gly	Arg
65					70					75					80
Lys	Pro	Lys	Val	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Arg	Ser	Cys	Lys
			85						90					95	
Cys	Ser														

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Cys	Cys	Leu	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Lys	Arg	Asp	Leu	Gly	Trp
1				5					10					15	

Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala Gly
 20 25 30
 Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val Leu
 35 40 45
 Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly Lys
 65 70 75 80
 Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys Lys
 85 90 95
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly Trp
 1 5 10 15
 Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser Gly
 20 25 30
 Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val Leu
 35 40 45
 Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys Cys
 50 55 60
 Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly Arg
 65 70 75 80
 Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys Lys
 85 90 95
 Cys Ser

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn
1           5           10           15
Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
20           25           30
Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe
35           40           45
His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
50           55           60
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
65           70           75           80
Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
85           90           95
Asn Met Ile Val Glu Glu Cys Gly Cys Ser
100          105

```

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
1           5           10           15
Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
20           25           30
Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
35           40           45
His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
50           55           60
Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
65           70           75           80
Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
85           90           95
Met Ile Val Glu Glu Cys Gly Cys Ala
100          105

```

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

Cys Arg Arg Val Lys Phe Gln Val Asp Phe Asn Leu Ile Gly Trp Gly
1           5           10           15
Ser Trp Ile Ile Tyr Pro Lys Gln Tyr Asn Ala Tyr Arg Cys Glu Gly
          20           25           30
Glu Cys Pro Asn Pro Val Gly Glu Glu Phe His Pro Thr Asn His Ala
          35           40           45
Tyr Ile Gln Ser Leu Leu Lys Arg Tyr Gln Pro His Arg Val Pro Ser
          50           55           60
Thr Cys Cys Ala Pro Val Lys Thr Lys Pro Leu Ser Met Leu Tyr Val
65           70           75           80
Asp Asn Gly Arg Val Leu Leu Glu His His Lys Asp Met Ile Val Glu
          85           90           95
Glu Cys Gly Cys Leu
          100

```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1           5           10           15
Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly
          20           25           30
Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
          35           40           45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala
          50           55           60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65           70           75           80
Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu
          85           90           95
Gly Cys Gly Cys Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
1           5           10           15
Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly
20           25           30
Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala
35           40           45
Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala
50           55           60
Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp
65           70           75           80
Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu
85           90           95
Gly Cys Gly Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asp
1           5           10           15
Asp Trp Ile Val Ala Pro Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly
20           25           30
Lys Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser Thr Asn His Ala
35           40           45
Val Val Gln Thr Leu Val Asn Asn Met Asn Pro Gly Lys Val Pro Lys
50           55           60
Ala Cys Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met Leu Tyr Leu
65           70           75           80

```

Asn Asp Gln Ser Thr Val Val Leu Lys Asn Tyr Gln Glu Met Thr Val
85 90 95

Val Gly Cys Gly Cys Arg
100

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

[illegible]

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Cys	Arg	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Gln
1				5					10					15	
Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	Gly
			20					25					30		
Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala
		35					40					45			

Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95
 Arg Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
 1 5 10 15

Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
 20 25 30
 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys
 50 55 60
 Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr
 65 70 75 80
 Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val
 85 90 95
 Lys Ala Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp His
 1 5 10 15
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser Gly
 20 25 30
 Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro Lys
 50 55 60
 Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr His
 65 70 75 80
 Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile Val
 85 90 95
 Lys Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
 1 5 10 15
 Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly
 20 25 30
 Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
 35 40 45
 Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile Pro
 50 55 60
 Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu Phe
 65 70 75 80
 Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met Thr
 85 90 95
 Val Glu Ser Cys Ala Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys Asp Val Gly Trp Gln
 1 5 10 15
 Asn Trp Val Ile Ala Pro Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly
 20 25 30
 Glu Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly Ser Asn His Ala
 35 40 45
 Ile Leu Gln Thr Leu Val His Ser Ile Glu Pro Glu Asp Ile Pro Leu
 50 55 60
 Pro Cys Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met Leu Phe Tyr
 65 70 75 80
 Asp Asn Asn Asp Asn Val Val Leu Arg His Tyr Glu Asn Met Ala Val
 85 90 95
 Asp Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly Trp His
1           5           10           15
Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr Cys Gln Gly
20           25           30
Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly Gly Pro Pro Ala
35           40           45
Leu Asn His Ala Val Leu Arg Ala Leu Met His Ala Ala Ala Pro Gly
50           55           60
Ala Ala Asp Leu Pro Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser
65           70           75           80
Val Leu Phe Phe Asp Asn Ser Asp Asn Val Val Leu Arg Gln Tyr Glu
85           90           95
Asp Met Val Val Asp Glu Cys Gly Cys Arg
100          105

```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```

Cys His Arg His Gln Leu Phe Ile Asn Phe Gln Asp Leu Gly Trp His
1           5           10           15
Lys Trp Val Ile Ala Pro Lys Gly Phe Met Ala Asn Tyr Cys His Gly
20           25           30
Glu Cys Pro Phe Ser Met Thr Thr Tyr Leu Asn Ser Ser Asn Tyr Ala
35           40           45
Phe Met Gln Ala Leu Met His Met Ala Asp Pro Lys Val Pro Lys Ala
50           55           60
Val Cys Val Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp
65           70           75           80
Ser Asp Lys Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp
85           90           95
Glu Cys Gly Cys Gly
100

```

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Cys Arg Arg Thr Ser Leu His Val Asn Phe Lys Glu Ile Gly Trp Asp
 1 5 10 15
 Ser Trp Ile Ile Ala Pro Lys Asp Tyr Glu Ala Phe Glu Cys Lys Gly
 20 25 30
 Gly Cys Phe Phe Pro Leu Thr Asp Asn Val Thr Pro Thr Lys His Ala
 35 40 45
 Ile Val Gln Thr Leu Val His Leu Gln Asn Pro Lys Lys Ala Ser Lys
 50 55 60
 Ala Cys Cys Val Pro Thr Lys Leu Asp Ala Ile Ser Ile Leu Tyr Lys
 65 70 75 80
 Asp Asp Ala Gly Val Pro Thr Leu Ile Tyr Asn Tyr Glu Gly Met Lys
 85 90 95
 Val Ala Glu Cys Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp Glu
 1 5 10 15
 Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His Gly
 20 25 30
 Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro Gly
 35 40 45
 Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala Gln
 50 55 60
 Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val Arg
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:170:

- (ii) MOLECULE TYPE: peptide

- [illegible]

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Cys	Glu	Leu	His	Asp	Phe	Ser	Leu	Ser	Phe	Ser	Gln	Leu	Lys	Trp	Asp
1				5					10					15	
Asn	Trp	Ile	Val	Ala	Pro	His	Ser	Tyr	Asn	Pro	Ser	Tyr	Cys	Lys	Gly
			20					25					30		
Asp	Cys	Pro	Ser	Ala	Val	Ser	His	Arg	Tyr	Gly	Ser	Pro	Val	His	Thr
		35					40					45			

Met Val Gln Asn Met Ile Tyr Glu Lys Leu Asp Pro Ser Val Pro Ser
 50 55 60
 Pro Ser Cys Val Pro Gly Lys Tyr Ser Pro Leu Ser Val Leu Thr Ile
 65 70 75 80
 Glu Pro Asp Gly Ser Ile Ala Tyr Lys Glu Tyr Glu Asp Met Met Ala
 85 90 95
 Thr Ser Cys Thr Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1 5 10 15
 Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
 20 25 30
 Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
 35 40 45
 Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
 50 55 60
 Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
 65 70 75 80
 His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly
 1 5 10 15
 Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys
 20 25 30

Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln
 35 40 45
 Arg Arg Arg Leu Arg Arg Glu Arg Val Arg Ala Gln Pro Cys Cys Arg
 50 55 60
 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Ala His Ser Arg
 65 70 75 80
 Tyr His Thr Val His Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
 85 90 95

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Leu Asp Leu Gln Glu Ala Ser Val Ala Asp Lys Leu Ser Phe Gly Lys
 1 5 10 15
 Met Ala Glu Thr Arg Gly Thr Trp Thr Pro His Gln Gly Asn Asn His
 20 25 30
 Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Leu Asp Leu Gln Glu Ala Pro Ala Ala Asp Glu Leu Ser Ser Gly Lys
 1 5 10 15
 Met Ala Glu Thr Gly Arg Thr Trp Lys Pro His Gln Gly Asn Asn Asn
 20 25 30
 Val Arg Leu Pro Arg
 35

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Cys Val Leu Thr Ala Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly
 1           5           10           15
Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys
          20           25           30
Glu Ser Ala Glu Thr Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg
          35           40           45
Ser Arg Arg Leu Thr Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro
          50           55           60
Val Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp Asp Asn Leu Val Tyr
          65           70           75           80
His Ile Leu Arg Lys His Ser Ala Lys Arg Cys Gly Cys
          85           90

```

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC      60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG      120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAAGA ATTCCTGGGG GCCTCCCGAC      180
TCCCCAATTC CTTCTCTCAA AGCCCTCACT TTGCCTTACA ATCCTACTCT ACCTTGCACT      240
AGGTAACAAC CATGTCCGTC TTCCAAGAGC CTTGGCTGGT TCATGCCGAC TGTGGAGCCT      300
GACCCTACCA GTGGCTGAGC TGGGCCTGGG CTATGCCTCG GAGGAGAAGG TCATCTTCCG      360
ATACTGTGCT GGCAGCTGTC CCCAAGAGGC CCGTACCCAG CACAGTCTGG TACTGGCCCCG      420
GCTTCGAGGG CGGGGTCGAG CCCATGGCCG ACCCTGCTGC CAGCCCACCA GCTATGCTGA      480
TGTGACCTTC CTTGATGATC AGCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCTGCAGC      540
TTGTGGCTGT GGTGGCTGAA GGAGGCCAGT CTGGTGTCTC AGAATCACAA GCATGAGACA      600
GGCTGGGCTT TGAAAGGCTC AGGTGACATT ACTAGAAATT TGCATAGGTA AAGATAAGAA      660

```


GGGAAAGGAC CAGGGGTTTT TTGTTTCTTT CTTTGCTTGC TTGTTAGTTT TTTTTTTTTT 720
TTT 723

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

AAAAAAAAA AAAAATACTAA CAAGCAAGCA AAGAAAGAAA CAAAAAACCC CTGGTCCTTT 60
 CCCTTCTTAT CTTTACCTAT GCAAATTTCT AGTAATGTCA CCTGAGCCTT TCAAAGCCCCA 120
 GCCTGTCTCA TGCTTGTGAT TCTGAGACAC CAGACTGGCC TCCTTCAGCC ACCACAGCCA 180
 CAAGCTGCAG CTGAGAGCTG AGGCAGCTGC TGCCAATGGT GCTGATCATC AAGGAAGGTC 240
 ACATCAGCAT AGCTGGTGGG CTGGCAGCAG GGTCGGCCAT GGGCTCGACC CCGCCCTCGA 300
 AGCCGGGCCA GTACCAGACT GTGCTGGGTA CGGGCCTCTT GGGGACAGCT GCCAGCACAG 360
 TATCGGAAGA TGACCTTCTC CTCCGAGGCA TAGCCCAGGC CCAGCTCAGC CACTGGTAGG 420
 GTCAGGCTCC ACAGTCGGCA TGAACCAGCC AAGGCTCTTG GAAGACGGAC ATG GTTGTTA 480
 CCTAGTGCAA GGTAGAGTAG GATTGTAAGG CAAAGTGAGG GCTTTGAGAG AAGGAATTGG 540
 GGAGTCGGGA GGCCCCCAGG AATTCTTACC CTGATGGGGC GTCCAGGTCC CTCTAGTCTC 600
 TGCCATCTTC CCAAATGAGA GCTTATCTGC CACAGAAGCC TCTTGAAGAT CAAGGACCCA 660
 GCCGAGGCTC GGGTGCAAGG ACAGGAGCAG CAGACACAGG ATCCGAAGTC TTCCTGCAGC 720
 CAT 723

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG 120
 GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA 180

```

GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG      240
GGCTATGCCT CGGAGGAGAA GGTCATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG      300
GCCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTGG AGCCCATGGC      360
CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT      420
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A              471

```

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG      60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC      120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG      180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCCTCC GAGGCATAGC CCAGGCCAG      240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG CTCTTGGAAG      300
ACGGACATGG TTGTTACCTT GATGGGGCGT CCAGGTCCCT CTAGTCTCTG CCATCTTCCC      360
AAATGAGAGC TTATCTGCCA CAGAAGCCTC TTGAAGATCA AGGACCCAGC CGAGGCTCGG      420
GTGCAAGGAC AGGAGCAGCA GACACAGGAT CCGAAGTCTT CCTGCAGCCA T              471

```

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```

ATGGCTGCAG GAAGACTTCG GATCCTGTGT CTGCTGCTCC TGTCTTGCA CCCGAGCCTC      60
GGCTGGGTCC TTGATCTTCA AGAGGCTTCT GTGGCAGATA AGCTCTCATT TGGGAAGATG      120
GCAGAGACTA GAGGGACCTG GACGCCCCAT CAGGGTAACA ACCATGTCCG TCTTCCAAGA      180

```

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TCTTGGAAGA CGGACATGGT TGTTACCCTG ATGGGGCGTC CAGGTCCCTC TAGTCTCTGC	60
CATCTTCCCA AATGAGAGCT TATCTGCCAC AGAAGCCTCT TGAAGATCAA GGACCCAGCC	120
GAGGCTCGGG TGCAAGGACA GGAGCAGCAG ACACAGGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GCCTTGGCTG GTTCATGCCG ACTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTGGGCCTG	60
GGCTATGCCT CGGAGGAGAA GGTCACTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GCCCGTACCC AGCACAGTCT GGTACTGGCC CGGCTTCGAG GGCGGGGTCG AGCCCATGGC	180
CGACCCTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA TCAGCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCTGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

TCAGCCACCA CAGCCACAAG CTGCAGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGCTG	60
ATCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAGGGTC GGCCATGGGC	120
TCGACCCCGC CCTCGAAGCC GGGCCAGTAC CAGACTGTGC TGGGTACGGG CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATGAC CTTCTCTCC GAGGCATAGC CCAGGCCAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG TCGGCATGAA CCAGCCAAGG C	291

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Leu Ser Leu
1           5           10           15

His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala
          20           25           30

Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr
          35           40           45

Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg Ala Leu Ala Gly
          50           55           60

Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
          65           70           75           80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
          85           90           95

Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
          100          105          110

Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
          115          120          125

Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His Trp Gln Gln Leu
          130          135          140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Cys Leu Leu Leu Leu Ser Leu
1           5           10           15

His Pro Ser Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Ser Val Ala
          20           25           30

```

Asp Lys Leu Ser Phe Gly Lys Met Ala Glu Thr Arg Gly Thr Trp Thr
 35 40 45

Pro His Gln Gly Asn Asn His Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Ala Leu Ala Gly Ser Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Ala Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Arg Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp Gln His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCTTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAAGA ATTCTTGGGG GCCTCCTAAC	180
TCTACAGTTC TTCCTCTCAA AGCCCTCACT TTGCCTCACA ATCCTATTCT ACCTTGCACT	240
AGGTAACAAC AATGTCCGCC TTCCAAGAGC CTTACCTGGT TTGTGCCGGC TGTGGAGCCT	300

GACCCTACCA GTGGCTGAGC TTGGCCTGGG CTATGCCTCA GAGGAGAAGA TTATCTTCCG	360
ATACTGTGCT GGCAGCTGTC CCCAAGAGGT CCGTACCCAG CACAGTCTGG TGCTGGCCCG	420
TCTTCGAGGG CAGGGTCGAG CTCATGGCAG ACCTTGCTGC CAGCCCACCA GCTATGCTGA	480
TGTGACCTTC CTTGATGACC ACCACCATTG GCAGCAGCTG CCTCAGCTCT CAGCCGCAGC	540
TTGTGGCTGT GGTGGCTGA	559

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAG	300
GCGGACATTG TTGTTACCTA GTGCAAGGTA GAATAGGATT GTGAGGCAAA GTGAGGGCTT	360
TGAGAGGAAG AACTGTAGAG TTAGGAGGCC CCCAAGAATT CTTACCCTGA TGGGGCTTCC	420
AGGTCCTTCC AGTCTCTGCC ATTTTCCAG ATGAGAGCTC ATCTGCCGCA GGAGCCTCTT	480
GAAGATCAAG GACCCAGCCA AGGCCAGGT GCAAGGACAG GAGCAGCAGA AACAAGATCC	540
GAAGTCTTCC TGCAGCCAT	559

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT	60
GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG	120
GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA	180

GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG 240
 GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG 300
 GTCCTGATCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC 360
 AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT 420
 TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG 60
 GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC 120
 TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG 180
 ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG 240
 CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG CTCTTGGAAG 300
 GCGGACATTG TTGTTACCCT GATGGGGCTT CCAGGTCCTT CCAGTCTCTG CCATTTTCCC 360
 AGATGAGAGC TCATCTGCCG CAGGAGCCTC TTGAAGATCA AGGACCCAGC CAAGGCCCAG 420
 GTGCAAGGAC AGGAGCAGCA GAAACAAGAT CCGAAGTCTT CCTGCAGCCA T 471

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

ATGGCTGCAG GAAGACTTCG GATCTTGTTT CTGCTGCTCC TGTCCTTGCA CCTGGGCCTT 60
 GGCTGGGTCC TTGATCTTCA AGAGGCTCCT GCGGCAGATG AGCTCTCATC TGGGAAAATG 120
 GCAGAGACTG GAAGGACCTG GAAGCCCCAT CAGGGTAACA ACAATGTCCG CCTTCCAAGA 180

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

TCTTGGAAGG CGGACATTGT TGTTACCCTG ATGGGGCTTC CAGGTCCTTC CAGTCTCTGC	60
CATTTTCCCA GATGAGAGCT CATCTGCCGC AGGAGCCTCT TGAAGATCAA GGACCCAGCC	120
AAGGCCCAGG TGCAAGGACA GGAGCAGCAG AAACAAGATC CGAAGTCTTC CTGCAGCCAT	180

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GCCTTACCTG GTTTGTGCCG GCTGTGGAGC CTGACCCTAC CAGTGGCTGA GCTTGGCCTG	60
GGCTATGCCT CAGAGGAGAA GATTATCTTC CGATACTGTG CTGGCAGCTG TCCCCAAGAG	120
GTCCGTACCC AGCACAGTCT GGTGCTGGCC CGTCTTCGAG GGCAGGGTCG AGCTCATGGC	180
AGACCTTGCT GCCAGCCCAC CAGCTATGCT GATGTGACCT TCCTTGATGA CCACCACCAT	240
TGGCAGCAGC TGCCTCAGCT CTCAGCCGCA GCTTGTGGCT GTGGTGGCTG A	291

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

TCAGCCACCA CAGCCACAAG CTGCGGCTGA GAGCTGAGGC AGCTGCTGCC AATGGTGGTG	60
GTCATCAAGG AAGGTCACAT CAGCATAGCT GGTGGGCTGG CAGCAAGGTC TGCCATGAGC	120
TCGACCCTGC CCTCGAAGAC GGGCCAGCAC CAGACTGTGC TGGGTACGGA CCTCTTGGGG	180
ACAGCTGCCA GCACAGTATC GGAAGATAAT CTTCTCCTCT GAGGCATAGC CCAGGCCAAG	240
CTCAGCCACT GGTAGGGTCA GGCTCCACAG CCGGCACAAA CCAGGTAAGG C	291

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
1           5           10           15
His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
20           25           30
Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
35           40           45
Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg Ala Leu Pro Gly
50           55           60
Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala Glu Leu Gly Leu
65           70           75           80
Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr Cys Ala Gly Ser
85           90           95
Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val Leu Ala Arg Leu
100          105          110
Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys Gln Pro Thr Ser
115          120          125
Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His Trp Gln Gln Leu
130          135          140
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

```

Met Ala Ala Gly Arg Leu Arg Ile Leu Phe Leu Leu Leu Leu Ser Leu
1           5           10           15
His Leu Gly Leu Gly Trp Val Leu Asp Leu Gln Glu Ala Pro Ala Ala
20           25           30

```

Asp Glu Leu Ser Ser Gly Lys Met Ala Glu Thr Gly Arg Thr Trp Lys
 35 40 45

Pro His Gln Gly Asn Asn Asn Val Arg Leu Pro Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Ala Leu Pro Gly Leu Cys Arg Leu Trp Ser Leu Thr Leu Pro Val Ala
 1 5 10 15
 Glu Leu Gly Leu Gly Tyr Ala Ser Glu Glu Lys Ile Ile Phe Arg Tyr
 20 25 30
 Cys Ala Gly Ser Cys Pro Gln Glu Val Arg Thr Gln His Ser Leu Val
 35 40 45
 Leu Ala Arg Leu Arg Gly Gln Gly Arg Ala His Gly Arg Pro Cys Cys
 50 55 60
 Gln Pro Thr Ser Tyr Ala Asp Val Thr Phe Leu Asp Asp His His His
 65 70 75 80
 Trp Gln Gln Leu Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 85 90 95

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear .

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 60
 GGCTACGCCT CAGAGGAGAA GGTCTCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT 120
 GCCCGCAGCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGT 180
 GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 240
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 291

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGGC      120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG      180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG      240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C                291
```

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG      60
GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT      120
GCCCGCACCC AGCATGGCCT GGCGCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCCACGGC      180
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC      240
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A                291
```

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG      60
```

GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG C	291

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG	60
GGCTGGGGCC CCGATGCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG	120
GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCC CTCTGCGCCGA	180
GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG	240
GGCTACGCCT CAGAGGAGAA GGTCATCTTC CGCTACTGCG CCGGCAGCTG CCCCCGTGGT	300
GGCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCACGGT	360
GGGCCCTGCT GCCGGCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC	420
TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A	471

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG	60
GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CACCGTGGGC	120
TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG	180
GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG	240
CTCTGCCACG GACAGGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG	300
GCGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTTCTAGA	360

CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG 420
 CTGCAGGGAC AGGAGCAGCA GAGAGCCCAG CAGGAACTTC CCTACGGCCA T 471

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCC TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACCGCC CCCTTGCCCC CCTGCGCCGA 180
 GCCCTGTCTG GTCCATGCCA GCTGTGGAGC CTGACCCTGT CCGTGGCAGA GCTAGGCCTG 240
 GGCTACGCCT CAGAGGAGAA GGTCACTTTC CGTACTGCG CCGGCAGCTG CCCCCGTGGT 300
 GCCCGCACCC AGCATGGCCT GGCCTGGCC CGGCTGCAGG GCCAGGGCCG AGCCACGGC 360
 GGGCCCTGCT GCCGGCCCAC TCGCTACACC GACGTGGCCT TCCTCGATGA CCGCCACCGC 420
 TGGCAGCGGC TGCCCCAGCT CTCGGCGGCT GCCTGCGGCT GTGGTGGCTG A 471

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TCAGCCACCA CAGCCGCAGG CAGCCGCCGA GAGCTGGGGC AGCCGCTGCC AGCGGTGGCG 60
 GTCATCGAGG AAGGCCACGT CGGTGTAGCG AGTGGGCCGG CAGCAGGGCC CGCCGTGGGC 120
 TCGGCCCTGG CCCTGCAGCC GGGCCAGCGC CAGGCCATGC TGGGTGCGGG CACCACGGGG 180
 GCAGCTGCCG GCGCAGTAGC GGAAGATGAC CTTCTCCTCT GAGGCGTAGC CCAGGCCTAG 240
 CTCTGCCACG GACAGGTCA GGCTCCACAG CTGGCATGGA CCAGACAGGG CTCGGCGCAG 300
 GCGGGCAAGG GGGCGGTGGG TGCCCAGCCA GGTCCCTCCA GCCTTTGCCA CCTGTTTACA 360
 CGAGAACTCT CCATCGGCCA CGGGAACCCC ACGGGCATCG GGGCCCCAGC CCTGTCCCAG 420
 CTGCAGGGAC AGGAGCAGCA GGGAGCCCAG CAGGAACTTC CCTACGGCCA T 471

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGC 69

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGA GAGCCCAGCA GGAACTTCCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
GGCTGGGGC 69

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GCCCCAGCCC TGTCCCAGCT GCAGGGACAG GAGCAGCAGG GAGCCCAGCA GGAAGTTCCC 60
TACGGCCAT 69

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCCGATGCCC GTGGGGTTCC CGTGGCCGAT GGAGAGTTCT CGTCTGAACA GGTGGCAAAG 60
GCTGGAGGGA CCTGGCTGGG CACCCACCGC CCCCTTGCCC GCCTGCGCCG A 111

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG G 111

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCT CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60

GGCTGGGGCC CCGATGCCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCC CCCTTGCCCCG CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG AGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ATGGCCGTAG GGAAGTTCCT GCTGGGCTCC CTGCTGCTCC TGTCCCTGCA GCTGGGACAG 60
 GGCTGGGGCC CCGATGCCCCG TGGGGTTCCC GTGGCCGATG GAGAGTTCTC GTCTGAACAG 120
 GTGGCAAAGG CTGGAGGGAC CTGGCTGGGC ACCCACC GCCC CCCTTGCCCCG CCTGCGCCGA 180

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TCGGCGCAGG CGGGCAAGGG GGCGGTGGGT GCCCAGCCAG GTCCCTCCAG CCTTTGCCAC 60
 CTGTTTCAGAC GAGAACTCTC CATCGGCCAC GGGAACCCCA CGGGCATCGG GGCCCCAGCC 120
 CTGTCCCAGC TGCAGGGACA GGAGCAGCAG GGAGCCCAGC AGGAACTTCC CTACGGCCAT 180

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

```

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
 1             5             10             15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20             25             30

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35             40             45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly
 50             55             60

Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu
 65             70             75             80

Gly Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser
 85             90             95

Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu
 100            105            110

Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg
 115            120            125

Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu
 130            135            140

Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly
 145            150            155

```

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

```

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Ser Leu
 1             5             10             15

Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala
 20             25             30

```

Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp
 35 40 45

Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu
 1 5 10 15

 Gln Leu Gly Gln Gly Trp Gly
 20

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Pro Asp Ala Arg Gly Val Pro Val Ala Asp Gly Glu Phe Ser Ser Glu
 1 5 10 15

 Gln Val Ala Lys Ala Gly Gly Thr Trp Leu Gly Thr His Arg Pro Leu
 20 25 30

 Ala Arg Leu Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Ala	Leu	Ser	Gly	Pro	Cys	Gln	Leu	Trp	Ser	Leu	Thr	Leu	Ser	Val	Ala
1				5					10					15	
Glu	Leu	Gly	Leu	Gly	Tyr	Ala	Ser	Glu	Glu	Lys	Val	Ile	Phe	Arg	Tyr
			20					25					30		
Cys	Ala	Gly	Ser	Cys	Pro	Arg	Gly	Ala	Arg	Thr	Gln	His	Gly	Leu	Ala
		35					40					45			
Leu	Ala	Arg	Leu	Gln	Gly	Gln	Gly	Arg	Ala	His	Gly	Gly	Pro	Cys	Cys
	50					55					60				
Arg	Pro	Thr	Arg	Tyr	Thr	Asp	Val	Ala	Phe	Leu	Asp	Asp	Arg	His	Arg
65					70					75					80
Trp	Gln	Arg	Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGCCAGCTGT	GGAGCCTGAC	CCTGTCCGTG	GCAGAGCTAG	GCCTGGGCTA	CGCCTCAGAG	60
GAGAAGGTCA	TCTTCCGCTA	CTGCGCCGGC	AGTGCCCCC	GTGGTGCCCG	CACCCAGCAT	120
GGCCTGGCGC	TGGCCCCGGCT	GCAGGGCCAG	GGCCGAGCCC	ACGGTGGGCC	CTGCTGCCGG	180
CCCACTCGCT	ACACCGACGT	GGCCTTCCTC	GATGACCGCC	ACCCTGGCA	GCGGCTGCCC	240
CAGCTCTCGG	CGGCTGCCTG	CGGCTGT				267

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu Gly
1 5 10 15
Tyr Ala Ser Glu Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser Cys
20 25 30

Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu Gln
 35 40 45

Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg Tyr
 50 55 60

Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu Pro
 65 70 75 80

Gln Leu Ser Ala Ala Ala Cys Gly Cys
 85

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Ala Leu Ser Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GTSASYGASY TGGGYCTGGG CTAY

24

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

TTYMGSTACT GCRSMGGCKC YTGC

24

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

RWAGGCSRTS G GKCKGCARC AKGS

24

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

MKCRCTCYARR AASGACASST C

21

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 168 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

CGGCTTGTGA CCGAGCTGGG CCTGGGCTAC GCCTCAGAGG AGAAGGTCAT CTCCGCTAC	60
TGCGCCGGCA GCTGCCCCCG TGGTGCCCGC ACCCAGCATG GCCTGGCGCT GGCCCGGCTG	120
CAGGGCCAGG GCCGAGCCCA CGGCGGGCCC TGCTGCCGCC CCATGGCC	168

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAGGAGAAGG TCATCTCCG

20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GCCGTGGGCT CGGCCCTGGC

20

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

AGAGGAGAAG GTCATCTTCC GCTA

24

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTCGGCCCTG GCCCTGCAGC

20

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

TGCAGCCGGG CCAGCGCCAG

20

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CGCGGATCCA TGCCTGGATT CGAGGGTGCA G

31

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CGCGGATCCA TGGCCGTAGG GAAGTTCCTG C

31

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCGC CACCACAGCC GCAGGCAGCC

60

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC

25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro
			5						10					15
Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
			20						25					30
Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser
			35						40					45
Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln
			50						55					60
Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly		
			65						70					

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids

}

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu
				5					10					15
Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly
				20					25					30
Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn
				35					40					45
Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala
				50					55					60
Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp
				65					70					75
Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg
				80					85					90
Cys	Gly	Cys												

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
				5					10					15	
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
			20					25					30		
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
			35				40					45			
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
			50			55				60					
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
			65			70			75					80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
			85					90							

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC

25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro
				5					10					15
Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg
				20					25					30
Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser
				35					40					45
Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln
				50					55					60
Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly		
				65					70					

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu
				5					10					15
Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly
				20					25					30
Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn
				35					40					45
Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala
				50					55					60
Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp
				65					70					75
Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg
				80					85					90

Cys Gly Cys

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
				5					10						15
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
				20					25					30	
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
				35					40					45	
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
				50					55					60	
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
				65					70					75	80
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85					90						

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG

59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC

25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro	
				5					10					15	
Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg	
				20					25					30	
Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	
				35					40					45	
Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln	
				50					55					60	
Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly			
				65					70						

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu			
				5					10					15			
Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly			
				20					25					30			
Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn			
				35					40					45			
Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala			
				50					55					60			
Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp			
				65					70					75			
Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg			
				80					85					90			

Cys Gly Cys

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly			
				5					10					15				
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys			
				20				25					30					
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg			
				35				40					45					
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro			
				50				55					60					
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr			
				65				70					75		80			
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys						
				85					90									

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCCCAAGCT TTTACTTGTC ATCGTCGTCC TTGTAGTCTC GAGGAAGGCC ACGTCGGTG 59

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAGCCACCA CAGCCGCAGG CAGCC 25

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Ser	Glu	Glu	Lys	Ile	Ile	Phe	Arg	Tyr	Cys	Ala	Gly	Ser	Cys	Pro	
				5					10					15	
Gln	Glu	Val	Arg	Thr	Gln	His	Ser	Leu	Val	Leu	Ala	Arg	Leu	Arg	
				20					25					30	
Gly	Gln	Gly	Arg	Ala	His	Gly	Arg	Pro	Cys	Cys	Gln	Pro	Thr	Ser	
				35					40					45	
Tyr	Ala	Asp	Val	Thr	Phe	Leu	Asp	Asp	His	His	His	Trp	Gln	Gln	
				50					55					60	
Leu	Pro	Gln	Leu	Ser	Ala	Ala	Ala	Cys	Gly	Cys	Gly	Gly			
				65					70						

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu
				5					10					15
Gly	Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly
				20					25					30
Ser	Cys	Glu	Ala	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn
				35					40					45
Leu	Ser	Arg	Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala
				50					55					60
Cys	Cys	Arg	Pro	Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp
				65					70					75
Asp	Ser	Leu	Val	Tyr	His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg
				80					85					90
Cys Gly Cys														

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Cys	Val	Leu	Thr	Ala	Ile	His	Leu	Asn	Val	Thr	Asp	Leu	Gly	Leu	Gly
				5					10						15
Tyr	Glu	Thr	Lys	Glu	Glu	Leu	Ile	Phe	Arg	Tyr	Cys	Ser	Gly	Ser	Cys
				20					25					30	
Glu	Ser	Ala	Glu	Thr	Met	Tyr	Asp	Lys	Ile	Leu	Lys	Asn	Leu	Ser	Arg
				35					40				45		
Ser	Arg	Arg	Leu	Thr	Ser	Asp	Lys	Val	Gly	Gln	Ala	Cys	Cys	Arg	Pro
				50			55				60				
Val	Ala	Phe	Asp	Asp	Asp	Leu	Ser	Phe	Leu	Asp	Asp	Asn	Leu	Val	Tyr
				65			70			75				80	
His	Ile	Leu	Arg	Lys	His	Ser	Ala	Lys	Arg	Cys	Gly	Cys			
				85					90						

*Sub
E14
cont*